

295899US0PCT.ST25  
SEQUENCE LISTING

<110> Kudo, Toshiaki  
Motoyama, Takayuki

<120> METHOD OF SCREENING FUNGUS-SPECIFIC ANTIMICROBIAL AGENT AND KIT  
THEREFOR

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<140> US 10/591,464  
<141> 2006-09-01

<150> PCT/JPO5/004272  
<151> 2005-03-04

<150> JP 2004-061273  
<151> 2004-04-04

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<170> PatentIn version 3.3

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 Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly Thr Glu Gly Arg Leu  
 420 425 430  
 Gly Gly Gln Ala Thr Val His Asp Val Gln Gly Thr Trp Arg Asp Leu  
 435 440 445  
 Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu Thr Thr Gln Val Arg  
 450 455 460  
 Glu Ile Ala Lys Val Thr Thr Ala Val Ala Lys Gly Asp Leu Thr Lys  
 465 470 475 480  
 Lys Ile Gly Val Glu Val Gln Gly Glu Ile Leu Asp Leu Lys Asn Thr  
 485 490 495  
 Ile Asn Thr Met Val Asp Arg Leu Gly Thr Phe Ala Phe Glu Val Ser  
 500 505 510  
 Lys Val Ala Arg Glu Val Gly Thr Asp Gly Thr Leu Gly Gly Gln Ala  
 515 520 525  
 Gln Val Asp Asn Val Glu Gly Lys Trp Lys Asp Leu Thr Glu Asn Val  
 530 535 540  
 Asn Thr Met Ala Ser Asn Leu Thr Ser Gln Val Arg Gly Ile Ser Thr  
 545 550 555 560  
 Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser Arg Lys Ile Glu Val  
 565 570 575  
 Glu Ala Lys Gly Glu Ile Leu Ile Leu Lys Glu Thr Ile Asn Asn Met  
 580 585 590  
 Val Asp Arg Leu Ser Ile Phe Cys Asn Glu Val Gln Arg Val Ala Lys  
 595 600 605  
 Asp Val Gly Val Asp Gly Ile Met Gly Gly Gln Ala Asp Val Ala Gly  
 610 615 620  
 Leu Lys Gly Arg Trp Lys Glu Ile Thr Thr Asp Val Asn Thr Met Ala  
 625 630 635 640

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Asn Asn Leu Thr Ala Gln Val Arg Ala Phe Gly Asp Ile Thr Asn Ala  
645 650 655

Ala Thr Asp Gly Asp Phe Thr Lys Leu Val Glu Val Glu Ala Ser Gly  
660 665 670

Glu Met Asp Glu Leu Lys Lys Ile Asn Gln Met Val Tyr Asn Leu  
675 680 685

Arg Asp Ser Ile Gln Arg Asn Thr Gln Ala Arg Glu Ala Ala Glu Leu  
690 695 700

Ala Asn Lys Thr Lys Ser Glu Phe Leu Ala Asn Met Ser His Glu Ile  
705 710 715 720

Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Gln Leu Thr Leu Asp  
725 730 735

Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu Asn Ile Val Asn Ser  
740 745 750

Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu Asp Leu Ser  
755 760 765

Lys Ile Glu Ala Arg Arg Met Val Ile Glu Glu Ile Pro Tyr Thr Leu  
770 775 780

Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu Ala Val Lys Glu Thr  
785 790 795 800

Glu Lys Phe Leu Asp Leu Thr Tyr Arg Val Asp His Ser Val Pro Asp  
805 810 815

His Val Val Gly Asp Ser Phe Arg Leu Arg Gln Ile Ile Leu Asn Leu  
820 825 830

Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly Glu Val Ser Leu Thr  
835 840 845

Ile Gln Lys Ala Ser Ser Val Gln Cys Ser Thr Glu Glu Tyr Ala Ile  
850 855 860

Glu Phe Val Val Ser Asp Thr Gly Ile Gly Ile Pro Ala Asp Lys Leu  
865 870 875 880

Asp Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp Gly Ser Met Thr Arg  
885 890 895

Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys Arg Leu Val  
900 905 910

Asn Leu Met Gly Gly Asp Val Trp Val Lys Ser Glu Tyr Gly Lys Gly  
915 920 925

Ser Lys Phe Phe Phe Thr Cys Val Val Arg Leu Ala Asn Asp Asp Ile  
930 935 940

Ser Leu Ile Ala Lys Gln Leu Asn Pro Tyr Lys Ser His Gln Val Leu  
945 950 955 960

Phe Ile Asp Lys Gly Arg Thr Gly His Gly Pro Glu Ile Ala Lys Met  
965 970 975

Leu His Gly Leu Gly Leu Val Pro Ile Val Val Asp Ser Glu Arg Asn  
980 985 990

Pro Ala Leu Glu Lys Ala Arg Ala Ala Gly Gln Ala Pro Tyr Asp Val  
995 1000 1005

Ile Ile Val Asp Ser Ile Glu Asp Ala Arg Arg Leu Arg Ser Val  
1010 1015 1020

Asp Asp Phe Lys Tyr Leu Pro Ile Val Leu Leu Ala Pro Val Val  
1025 1030 1035

His Val Ser Leu Lys Ser Cys Leu Asp Leu Gly Ile Thr Ser Tyr  
1040 1045 1050

Met Thr Thr Pro Cys Gln Leu Ile Asp Leu Gly Asn Gly Met Val  
1055 1060 1065

Pro Ala Leu Glu Asn Arg Ala Thr Pro Ser Leu Ala Asp Asn Thr  
1070 1075 1080

Lys Ser Phe Glu Ile Leu Leu Ala Glu Asp Asn Thr Val Asn Gln  
1085 1090 1095

Arg Leu Ala Val Lys Ile Leu Glu Lys Tyr His His Val Val Thr  
1100 1105 1110

Val Val Gly Asn Gly Glu Glu Ala Val Glu Ala Val Lys Arg Lys  
1115 1120 1125

Lys Phe Asp Val Ile Leu Met Asp Val Gln Met Pro Ile Met Gly  
1130 1135 1140

Gly Phe Glu Ala Thr Ala Lys Ile Arg Glu Tyr Glu Arg Ser Leu  
1145 1150 1155

Gly Ser Gln Arg Thr Pro Ile Ile Ala Leu Thr Ala His Ala Met  
1160 1165 1170

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Met Gly Asp Arg Glu Lys Cys Ile Gln Ala Gln Met Asp Glu Tyr  
1175 1180 1185

Leu Ser Lys Pro Leu Gln Gln Asn His Leu Ile Gln Thr Ile Leu  
1190 1195 1200

Lys Cys Ala Thr Leu Gly Gly Gln Leu Leu Glu Lys Asn Arg Glu  
1205 1210 1215

Arg Glu Leu Thr Arg Ala Ala Asp Ala Val Thr Gly Gly Arg Arg  
1220 1225 1230

Asp Asn Gly Met Tyr Ser Ala Ser Gln Ala Ala Gln His Ala Ala  
1235 1240 1245

Leu Arg Pro Pro Leu Ala Thr Arg Gly Leu Thr Ala Ala Asp Ser  
1250 1255 1260

Leu Val Ser Gly Leu Glu Ser Pro Ser Ile Val Thr Ala Asp Lys  
1265 1270 1275

Glu Asp Pro Leu Ser Arg Ala Arg Ala Ser Leu Ser Glu Pro Asn  
1280 1285 1290

Ile His Lys Ala Ser  
1295